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 YOU, MING
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<120> GENE EXPRESSION AND POLYMORPHISMS ASSOCIATED WITH LUNG
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<140> 10/595,571

<141> 2006-04-27

<150> PCT/US04/35690

<151> 2004-10-27

<150> 60/514,673

<151> 2003-10-27

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<170> PatentIn Ver. 3.3

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 Ala Glu Arg Leu Arg Leu Met Gln Glu Glu Glu Arg Arg Leu Lys
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 35 40 45
 Leu Glu Ile Gln Arg Ile Glu Arg Glu Lys Trp Xaa Leu Leu Glu Lys
 50 55 60
 Lys Asp Leu Glu Arg Arg Ser Gln Glu Leu Glu Glu Leu Ala Leu Leu
 65 70 75 80
 Glu Gly Cys Phe Pro Glu Ala Glu Lys Gln Lys Arg Glu Ile Arg Ala
 85 90 95
 Leu Ala Gln Trp Lys His Tyr Thr Glu Cys Asp Gly Ser Pro Asp Pro
 100 105 110
 Trp Val Ala Gln Glu Met Asn Thr Phe Ile Ser Leu Trp Glu Glu Glu
 115 120 125
 Lys Asn Gln Ala Phe Glu Gln Val Met Glu Lys Ser Lys Leu Val Leu
 130 135 140
 Ser Leu Ile Glu Lys Val Lys Leu Ile Leu Leu Glu Thr Pro Thr Tyr
 145 150 155 160
 Glu Leu Asp His Arg Thr Val Leu Gln His Gln Gly Ser Ile Leu Arg
 165 170 175
 Leu Gln Glu Leu Leu Ser Leu Lys Ile Asn Val Ala Thr Glu Leu Leu
 180 185 190
 Leu Arg Gln Ala Ser Asn Leu Ala Asp Leu Asp Thr Gly Asn Met Glu
 195 200 205
 Lys Ile Ile Lys Asp Glu Asn Val Thr Leu Tyr Val Trp Ala Asn Leu
 210 215 220
 Lys Lys Asn Pro Arg His Arg Ser Val Arg Phe Ser Glu Thr Gln Ile
 225 230 235 240

Gly	Phe	Glu	Ile	Pro	Arg	Ile	Leu	Ala	Thr	Ser	Asn	Val	Ala	Leu	Arg	245	250	255
Leu	Leu	His	Thr	Arg	Tyr	Asp	His	Ile	Thr	Pro	Leu	Phe	Pro	Ile	Ala	260	265	270
Val	Thr	Glu	Gln	Asn	Gln	Asn	Pro	Val	Gly	Ala	Glu	Gln	Val	Asn	Val	275	280	285
Glu	Glu	Ser	Thr	Glu	Lys	Ala	Met	Thr	Glu	Glu	Lys	Leu	Phe	Thr	Glu	290	295	300
Glu	Lys	Ala	Ala	Asn	Glu	Asp	Glu	Gln	Pro	Lys	Ala	Glu	Gln	Glu	Arg	305	310	315
Glu	Leu	Asn	Leu	Val	Gln	Glu	Glu	Asn	Lys	Tyr	Glu	Ala	Ile	Glu	Asn	325	330	335
Thr	Val	Leu	Gln	Arg	Thr	Ser	Asp	Ser	Glu	Gly	Glu	Asp	Ser	Gln	Thr	340	345	350
Thr	Gln	Leu	Glu	Leu	Glu	Met	Lys	Leu	Leu	Ser	Glu	Ala	Val	Leu	Ala	355	360	365
Ala	Gln	Leu	Gln	Leu	Val	Glu	Asn	Val	Val	Glu	Leu	Pro	Glu	Ala	Ser	370	375	380
Gln	Ala	Tyr	Lys	Val	Asp	Leu	Cys	His	Phe	Ser	Thr	Leu	Gly	Gly	Val	385	390	395
Tyr	His	Leu	Asp	Val	Leu	Glu	Leu	Pro	Pro	Gln	Cys	Lys	Pro	Val	Lys	405	410	415
Gly	Trp	Val	Leu	Val	Glu	Ile	Leu	Gln	Glu	Gly	Leu	Gln	Arg	Phe	Ile	420	425	430
Tyr	Pro	Pro	Asp	Thr	Thr	Glu	Glu	Pro	Asp	Pro	Asp	Val	Thr	Phe	Pro	435	440	445
Pro	Ile	Glu	Val	Thr	Leu	Glu	Ile	His	Lys	Ser	Val	Ile	Phe	Phe	Glu	450	455	460
Arg	Pro	Arg	Val	Val	Arg	Trp	Asp	Asn	Glu	Gly	Lys	Phe	Trp	Arg	Ser	465	470	475
Asp	Gly	Ile	Ser	Ser	Val	Tyr	Tyr	Asn	Arg	Glu	Asp	Arg	Leu	Leu	Thr	485	490	495
Phe	Ser	Met	Asp	Thr	Leu	Gly	Pro	Val	Thr	Leu	Ile	Gln	Asp	Ala	His	500	505	510
Val	Asn	Met	Pro	Tyr	Gln	Ser	Trp	Glu	Met	Ser	Pro	Gln	Gly	Met	Asn	515	520	525
Lys	Val	Leu	Leu	Ile	Val	Lys	Thr	Val	Phe	Met	Glu	Leu	Gln	Ile	Tyr	530	535	540

Ile Lys Glu Asn Leu Cys Met Leu Ala Ser Val Lys Leu Arg Gly Lys
 545 550 555 560
 Gly Leu Glu Phe His Leu Lys Gly Lys Trp Met Ala Pro Ile Pro Phe
 565 570 575
 Ile Leu Ala Leu Lys Glu Ala Gly Leu Asn Ile Phe Pro Ala Val Tyr
 580 585 590
 Ser His Phe Tyr Val Val Ile Asn Asn Lys Val Pro Gln Val Glu Leu
 595 600 605
 Lys Ala Tyr Arg Gln Met Ala Leu Leu Ser Ser Ala Phe Ser Phe Gly
 610 615 620
 Trp Ser Lys Trp Asn Met Val Cys Asn Ser Thr Arg Val Val Ile Arg
 625 630 635 640
 Val Arg Glu Gln Leu Ser Glu Glu Thr Glu His His Thr Trp Ser Leu
 645 650 655
 Leu Met Phe Ser Gly Asp Arg Ala Gln Met Leu Lys Met Gln Glu Glu
 660 665 670
 Asn Asp Lys Phe Ser Glu Ala Leu Arg Glu Gly Thr Glu Phe His Ser
 675 680 685
 Thr Leu Tyr His Met Met Lys Asp Phe Ala Ser Pro Val Ala Met Glu
 690 695 700
 Arg Val Arg His Ser Asn Cys Gln Phe Ile Asp Ser Val Cys Tyr Met
 705 710 715 720
 Leu Leu Ser Ile Arg Val Leu Ser Tyr Ser
 725 730

<210> 22
 <211> 716
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (185)
 <223> Variable amino acid

<400> 22
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 20 25 30
 Arg Leu Lys Tyr Glu Lys Glu Glu Met Glu Arg Leu Glu Ile Gln Arg
 35 40 45

Ile	Glu	Lys	Glu	Lys	Trp	His	Arg	Leu	Glu	Ala	Lys	Asp	Leu	Glu	Arg	50	55	60
Arg	Asn	Glu	Glu	Leu	Glu	Glu	Leu	Tyr	Leu	Leu	Glu	Arg	Cys	Phe	Pro	65	70	75
Glu	Ala	Glu	Lys	Leu	Lys	Gln	Glu	Thr	Lys	Leu	Leu	Ser	Gln	Trp	Lys	85	90	95
His	Tyr	Ile	Gln	Cys	Asp	Gly	Ser	Pro	Asp	Pro	Ser	Val	Ala	Gln	Glu	100	105	110
Met	Asn	Thr	Phe	Ile	Ser	Leu	Trp	Lys	Glu	Lys	Thr	Asn	Glu	Thr	Phe	115	120	125
Glu	Glu	Val	Ile	Glu	Lys	Ser	Lys	Val	Val	Leu	Asn	Leu	Ile	Glu	Lys	130	135	140
Leu	Lys	Phe	Ile	Leu	Leu	Glu	Thr	Pro	Pro	Cys	Asp	Leu	Gln	Asp	Lys	145	150	155
Asn	Ile	Ile	Gln	Tyr	Gln	Glu	Ser	Ile	Leu	Gln	Leu	Gln	Glu	Leu	Leu	165	170	175
His	Leu	Lys	Phe	Gly	Val	Ala	Thr	Xaa	Ile	Leu	Leu	Lys	Gln	Ala	Ser	180	185	190
Thr	Leu	Ala	Asp	Leu	Asp	Ser	Gly	Asn	Met	Glu	Lys	Val	Ile	Lys	Asp	195	200	205
Glu	Asn	Val	Thr	Leu	Tyr	Val	Trp	Ala	Asn	Leu	Lys	Lys	Asn	Pro	Arg	210	215	220
His	Arg	Ser	Val	Arg	Phe	Ser	Glu	Thr	Gln	Ile	Gly	Phe	Glu	Ile	Pro	225	230	235
Arg	Ile	Leu	Ala	Thr	Ser	Asp	Ile	Ala	Val	Arg	Leu	Leu	His	Thr	His	245	250	255
Tyr	Asp	His	Val	Ser	Ala	Leu	His	Pro	Val	Ser	Thr	Pro	Ser	Lys	Glu	260	265	270
Tyr	Thr	Ser	Ala	Val	Thr	Glu	Leu	Val	Lys	Asp	Asp	Val	Lys	Asn	Val	275	280	285
Glu	Lys	Ala	Ile	Ser	Lys	Glu	Val	Glu	Glu	Glu	Ser	Lys	Gln	Gln	Glu	290	295	300
Arg	Gly	Ser	His	Leu	Ile	Gln	Glu	Glu	Glu	Ile	Lys	Val	Glu	Glu	Glu	305	310	315
Gln	Gly	Asp	Ile	Glu	Val	Lys	Met	Ser	Ser	Ala	Glu	Glu	Glu	Ser	Glu	325	330	335
Ala	Ile	Lys	Cys	Glu	Arg	Glu	Met	Lys	Val	Leu	Ser	Glu	Thr	Val	Ser	340	345	350

Ala	Ala	Gln	Leu	Leu	Leu	Val	Glu	Asn	Ser	Ser	Glu	Lys	Pro	Asp	Phe
		355					360					365			
Phe	Glu	Asp	Asn	Val	Val	Asp	Leu	Cys	Gln	Phe	Thr	Thr	Leu	Gly	Gly
	370					375					380				
Val	Tyr	His	Leu	Asp	Ile	Leu	Glu	Leu	Pro	Pro	Gln	Cys	Lys	Pro	Val
385					390					395					400
Lys	Gly	Trp	Met	Ile	Val	Glu	Ile	Leu	Lys	Glu	Gly	Leu	Gln	Lys	Tyr
			405						410					415	
Thr	Tyr	Pro	Pro	Glu	Thr	Thr	Glu	Glu	Phe	Glu	Thr	Glu	Asn	Ala	Phe
			420					425					430		
Pro	Pro	Ile	Glu	Val	Thr	Leu	Glu	Val	His	Glu	Asn	Val	Ile	Phe	Phe
		435					440					445			
Glu	Asp	Pro	Val	Val	Val	Arg	Trp	Asp	Ala	Glu	Gly	Lys	His	Trp	Arg
	450					455					460				
Thr	Asp	Gly	Ile	Ser	Asn	Val	Ser	Tyr	Lys	Pro	Lys	Glu	Arg	Leu	Val
465					470					475					480
Thr	Phe	Ser	Leu	Asp	Thr	Phe	Gly	Pro	Val	Thr	Leu	Ile	Gln	Asp	Ala
				485					490					495	
His	Ile	Asn	Met	Pro	Tyr	Gln	Ser	Trp	Glu	Leu	Arg	Pro	Leu	Asp	Val
			500					505					510		
Asn	Lys	Val	Leu	Leu	Thr	Val	Thr	Thr	Val	Phe	Thr	Glu	Ile	Gln	Ile
		515					520					525			
Gln	Ile	Lys	Glu	Asn	Leu	Cys	Met	Leu	Ser	Ser	Ile	Lys	Leu	Lys	Asp
	530					535					540				
Lys	Lys	His	Ile	Ser	Ile	Leu	Glu	Gly	Thr	Trp	Met	Thr	Pro	Ile	Pro
545					550					555					560
Phe	Ile	Ile	Ala	Leu	Lys	Glu	Ala	Gly	Leu	Asn	Ile	Phe	Pro	Thr	Arg
			565					570						575	
His	Ser	His	Phe	Tyr	Val	Ile	Ile	Asn	Asn	Lys	Val	Pro	Leu	Val	Glu
			580					585					590		
Val	Lys	Ala	Tyr	Arg	Gln	Met	Ala	Leu	Leu	Ser	Ser	Ala	Phe	Ala	Phe
		595					600					605			
Gly	Trp	Ser	Lys	Trp	Asn	Leu	Leu	Cys	Asn	Ser	Thr	Lys	Val	Val	Phe
	610					615					620				
Lys	Val	Arg	Glu	His	Leu	Thr	Glu	Glu	Cys	Thr	Glu	Asn	Pro	Asn	Trp
625					630					635					640
Ala	Leu	Leu	Met	Phe	Ser	Gly	Asp	Arg	Ala	Gln	Arg	Leu	Lys	Ile	Lys
				645					650					655	

Glu Glu Ser Glu Ala Phe Ser Glu Ala Leu Lys Glu Glu Thr Glu Phe
660 665 670

His Ser Thr Leu Tyr His Met Val Lys Asp Phe Ala Ser Glu Glu Ala
675 680 685

Met Glu Lys Val Arg Ser Ser Asn Cys Gln Phe Val Asn Ser Val Cys
690 695 700

His Met Leu Leu Ser Thr Arg Leu Leu Ser Tyr Ser
705 710 715

<210> 23

<211> 737

<212> PRT

<213> Ciona intestinalis

<400> 23

Met Pro Pro Lys Ser Pro Asn Arg Ser Gly Lys Ser Thr Pro Thr Arg
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Gly Arg Pro Gly Glu Lys Lys Asp Glu Glu Lys Leu Leu Gln Asp Glu
20 25 30

Glu Glu Glu Arg Leu Arg Leu Glu Gln Glu Glu Lys Ala Arg Gln Glu
35 40 45

Lys Glu Ala Arg Glu Lys Leu Glu Gln Glu Arg Arg Ala Glu Leu Asp
50 55 60

Thr Lys Lys Asp Lys Gln Val Phe Glu Thr Asn Ile Glu Leu Gly Ala
65 70 75 80

Val Lys Leu Glu Val Glu Gln Val Lys Asn Asp Lys Leu Ala His Ala
85 90 95

Glu Trp Asn Arg Tyr Met Lys Cys Asp Gly Lys Pro Asp Pro Thr Ser
100 105 110

Val Lys Glu Ile Asn Thr Phe Ile Ser Leu Ser His Glu Lys Gly Ser
115 120 125

Pro Asp Val Asn Ile Val Leu Glu Asp Ala Lys Leu Ile Leu Ser Leu
130 135 140

Ile Ser Asp Leu Asn Glu Leu Leu Glu Asp Phe Thr Pro Glu Glu Phe
145 150 155 160

Glu Gln Lys Val Asp Ser Tyr Arg Gln Thr Ile Leu Ser Leu Gln Asp
165 170 175

Leu Leu Leu Asn Arg Tyr Asn Glu Ala Thr Leu Lys Met Leu Lys Glu
180 185 190

Ala Ser Tyr Glu Ala Asp Ser Glu Ser Gly Asn Leu Gln Lys Val Val
195 200 205

Asp	Gly	Glu	Asn	Glu	Thr	Ile	Met	Leu	Trp	Ala	Asn	Leu	Asn	Lys	Asn		
210						215					220						
Pro	Arg	Phe	Lys	Leu	Phe	Glu	Phe	Glu	Asn	Glu	Lys	Ile	Ser	Phe	Glu		
225					230					235					240		
Leu	Pro	Lys	Val	Leu	Ala	Met	Ala	Asp	Ile	Ala	Val	Arg	Ile	Leu	Arg		
			245						250					255			
Thr	Lys	Phe	Asp	His	Tyr	Ser	His	Gln	Cys	Thr	Thr	Phe	Leu	Pro	Lys		
			260					265					270				
Lys	Lys	Lys	Val	Lys	Asp	Glu	Glu	Pro	Ile	Pro	Glu	Glu	Pro	Pro	Lys		
		275					280					285					
Pro	Glu	Asp	Ala	Glu	Glu	Val	Glu	Val	Lys	Gly	Asp	Glu	Glu	Asn	Gly		
290						295					300						
Glu	Asp	Ala	Lys	Ser	Val	Val	Glu	Glu	Gly	Arg	Gln	Ser	Lys	Gln	Ser		
305					310					315					320		
Asn	Glu	Pro	Gly	Leu	Val	Asn	Glu	Gly	Glu	Lys	Glu	Glu	Glu	Thr	Lys		
			325						330					335			
Lys	Asp	Glu	Asn	Glu	Gly	Glu	Lys	Glu	Asp	Ala	Val	Lys	Thr	Pro	Asp		
			340					345					350				
Val	Gln	Ile	Glu	Ile	Glu	Asp	Asp	Glu	Glu	Glu	Ile	Leu	Asp	Pro	Asp		
		355					360					365					
Val	Val	Asp	Leu	Arg	Gln	Phe	Ser	Pro	Leu	Gly	Gly	Val	Tyr	His	Val		
	370					375					380						
Asp	Leu	Leu	Lys	Thr	Pro	Pro	Gln	Pro	Asn	Ile	Val	Arg	Gly	Trp	Thr		
385					390					395					400		
Leu	Thr	Gln	Ile	Ile	Asp	Lys	Pro	Leu	Ser	Thr	Val	Lys	Tyr	Pro	Ser		
			405						410					415			
Asp	Asn	Pro	Asn	Thr	Gly	Arg	Ser	Ser	Ser	Arg	Val	Ala	Ser	Ala	Asn		
			420					425					430				
Pro	Glu	Gly	Arg	Asp	Glu	Gly	Ser	Pro	Ser	Lys	Thr	Pro	Leu	Glu	Gln		
		435					440					445					
Gln	Gln	Pro	Pro	Ile	Gly	Leu	Thr	Phe	Ala	Leu	Pro	Ser	Asn	Val	Met		
		450				455					460						
Phe	Phe	Glu	Glu	Pro	Gln	Val	Ala	Ser	Trp	Asp	Ser	Ser	Asp	Lys	His		
465					470					475					480		
Trp	Lys	Thr	Ser	Gly	Ile	Thr	Asp	Thr	Asn	Phe	Asp	Glu	Glu	Asn	Arg		
			485					490						495			
Lys	Leu	Leu	Phe	Lys	Thr	Gln	Glu	Phe	Gly	Thr	Phe	Cys	Leu	Met	Gln		
			500					505					510				

Asp Ser His Leu Asn Met Pro Phe Gln Ser Trp Glu Leu Lys Pro Lys
 515 520 525
 Gly Thr Asn Ser Thr Val Leu Thr Ile Thr Ala Ala Ile Ala Glu Val
 530 535 540
 Glu Ile Glu Val Lys Asp Ser Lys Cys Arg Leu Asn Ala Pro Ala Glu
 545 550 555 560
 Asp Pro Pro Lys Glu Leu Ser Gly Leu Tyr Gly Lys Trp Met Ala Val
 565 570 575
 Pro Lys Leu Ile Ala Ala Met Arg Asp Ala Gly Val Asn Val Phe Pro
 580 585 590
 Ala Glu Asp Ser His Lys Phe Val Ser Ile Gln Ser Lys Glu Val Asp
 595 600 605
 Leu Glu Arg Val Tyr Glu Gln Met Ala Ile Leu Ser Ser Thr Phe Ala
 610 615 620
 Phe Ser Trp Ser Lys Trp Asn Asn Asp Ala Gly Ser Lys Gln Val Ile
 625 630 635 640
 Ile Gln Ile Ala Pro Cys Leu Ile Lys Glu Asn Val Pro Arg Asp Ala
 645 650 655
 Val Ser Asp Asp Asp Trp Ser Ile Phe Ser Val Ser Asp Asp Met Ser
 660 665 670
 Tyr Lys Leu Ala Leu Ser Glu Tyr Asp Glu Glu Phe Ala Asp Val Val
 675 680 685
 Ala Lys Gly Ala Thr Tyr His Cys Asp Leu Leu His Ala Gln Tyr Glu
 690 695 700
 Arg Gln Pro Leu Lys Thr Ala Thr Lys Asn Cys Trp Asn Asn Ser Pro
 705 710 715 720
 Lys Asn His Lys Thr Arg Thr Ser Phe Ser Phe Thr Arg Leu Pro His
 725 730 735
 Tyr

<210> 24
 <211> 229
 <212> PRT
 <213> Rattus sp.

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 20 25 30

Val Thr Thr Val Phe Ile Glu Leu Gln Ile His Ile Lys Glu Thr His
 35 40 45

Cys Met Leu Ala Ala Val Lys Leu Lys Gly Lys Ser Arg Glu Leu Arg
 50 55 60

Val Ile Gly Lys Trp Met Thr Pro Ile Pro Phe Ile Leu Ala Leu Lys
 65 70 75 80

Glu Ala Gly Leu Asn Ile Phe Pro Ala Val Tyr Ser His Phe Tyr Val
 85 90 95

Val Val Asn Asn Lys Asn Pro Gln Met Glu Leu Lys Ala Tyr Arg Gln
 100 105 110

Met Ala Leu Leu Ser Ser Ala Phe Ser Phe Gly Trp Ser Lys Trp Asn
 115 120 125

Met Val Cys Asn Ser Thr Arg Val Val Phe Arg Val Arg Glu His Ile
 130 135 140

Ser Glu Glu Glu Glu Gln Asn Thr Trp Ala Leu Leu Met Phe Ser Gly
 145 150 155 160

Asp Arg Ala Gln Met Leu Lys Met Gln Glu Glu Ser Asp Gln Phe Ser
 165 170 175

Glu Thr Leu Arg Glu Gly Ser Glu Phe His Ser Thr Leu Tyr His Met
 180 185 190

Met Lys Asp Phe Ala Ser Pro Glu Ala Thr Glu Lys Val Arg His Ser
 195 200 205

Asn Cys Gln Phe Ile Asp Ser Val Cys Tyr Met Leu Leu Ser Val Arg
 210 215 220

Val Leu Ser Tyr Ser
 225

<210> 25

<211> 2417

<212> DNA

<213> Homo sapiens

<400> 25

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 aatactgaat tatcgaacac ttgccaggca cttcagcaga agacaaggaa actgaagaag 360
 cttttttagat gaggaatttc ctactatga ttccctgtcc tgcgcatatg caattcaaca 420
 acctcttcaa gaaaaattga agcagtgttg ccacaaacta tatggtggtc aagaagcaag 480
 aatacatcag acacccttga ccttgaaaca tacgtgctgg tacacacctc tgctggatgc 540
 cttatctctg gatagtttta cagcagttcc aaccctggaa tcaacacctt tctcaggtgt 600
 agccaaccaa atccacactc tgtgtgaaag gccacatat ggagaagtaa aggatggtgc 660
 tttggatgta aaaagacaac acaagtgcc aggcccccaca agtggcccca gccacaggaac 720

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acacacttca tgcacagacg gtactataac ttcaagtgat cctggattag aaattctgaa 900
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ttctctacga agagtgacta ttgcctcttt acccagaaat attggaatg caggaatggg 1740
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agaaacagta gaaaggacaa ggaagccaag tctttctgaa aagaaaaata atccatcaaa 1980
gtgggatgtc tcttcagttt atgacacaat agcttctctg gcaacaaatc tcaagtcctc 2040
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gcaagaggac tcatggacgt ctctagaaca tatcttgtgg ccatttacca gactccgaca 2220
caatgggcca ccaccagtgt gacagcagga catcctaata tatggatctt gatttttaag 2280
tttcagtatc tgaacttcgt aaattagtaa ctttttagctg ggaaagtata gcatgaaacc 2340
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<210> 26
 <211> 2263
 <212> DNA
 <213> Mus sp.

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<400> 26
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gcatccagcg cccttcccgc ggctcaaacc caggetgacc tgtgcatatg ggtcaggggg 180
atcaggatgg ggctgcgca tgaggcaagc ctctgctaca agaactagag gaagcgattc 240
cagaaggaga tcacagtccc cagcactact cagactcagg agctgaagac caggggcgtt 300
cagtatgcct gtgtcttgac ggctcacag caattccaag gctagaactg acacctatct 360
catgtgccag aaactcagcc catgctctgt gtaaaaggtc cccagagca ggaaccagaa 420
gatggggctt tggacgtgac aagagggtgc cagtgcacc tccccacgga aggtccatc 480
ttgggacagg agcttctaga ctgtaccaga atgaacgagg accagagtag agacgagaat 540
ggtgctgacc acttgattc cgagagcccg tcacagctca gggagtatct cacacagcca 600
tcgtctgaac agacttcac ctcgagagc actgtgacgt caagtgagtc tggatcagac 660
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acgagtgtgg gcgtggccaa ggctgcatcc cagctggaag caggagagga actcagaacc 840
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gcatctgtga agctcgtaa ctttcagcag agtgaaaaca cttcagctaa tgagaaggaa 960
gtgggggcag agttcctcag gttatctttg ggaacttaag gtgactgggt tacattggag 1020
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aacatgcaca ttttgtacat tgtgctttct tttgtgggac atatgcagtg tgatccagtt 5100
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accactcttt taattgaaat taacttttaa atgtttatag gagtatgtgc tgtgaagtga 5220
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aaaatagtta cagtgacaaa aaaaaaaaaa aa 5312

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<210> 31
 <211> 570
 <212> DNA
 <213> Mus sp.

```

<400> 31
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aggaaacaaag tagtaattga tggagaaacc tgtctcttgg atattctcga cacagcaggt 180
caagaggagt acagtgcaat gagggaccag tacatgagaa ctggggaggg ctttctttgt 240
gtatttgcca taaataatac taaatcattt gaagatattc accattatag agaacaaatt 300
aaaagagtaa aggactctga agatgtgcct atggtcctgg tagggaataa gtgtgatttg 360
ccttctagaa cagtagacac gaaacaggct caggagttag caaggagtta cgggattccg 420
ttcattgaga cctcagcaaa gacaagacag agagtggagg atgcttttta tacattggtg 480
agagagatcc gacgatcac attgaaaaaa atcagcaaaag aagaaaagac tcctggctgt 540
gtgaaaatta aaaaatgcgt tataatgttaa 570

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<210> 32
 <211> 1567
 <212> DNA
 <213> Mus sp.

<400> 32
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 gaaggcggcg gcgggagcct gaggcgcggc ggctccgcgg cgcggagaga ggctgtctga 180
 aaatgactga gtataaaact gtggtggttg gagctgggtg cgtaggcaag agcgctctga 240
 cgatacagct aattcagaat cactttgttg atgagtaaga ccctacgata gaggactcct 300
 acaggaaaac agtagtaatt gatggagaaa cctgtctctt ggatattctc gacacagcag 360
 gtcaagagga gtacagtgc atgagggacc agtacatgag aactggggag ggctttcttt 420
 gtgtatttgc cataaataat actaaatcat ttgaagatat tcaccattat agagaacaaa 480
 ttaaaaaggt aaaggactct gaagatgtgc ctatggtcct ggtagggaat aagtgtgatt 540
 tgccttctag aacagtagac acgaaacagg ctcaggagtt agcaaggagt tacgggattc 600
 cgttcattga gacctcagca aagacaagac aggggtgttg ccatgccttc taccatttag 660
 tccgagaaat tcgaaaacat aaagaaaaga tgggaagaag aagaagaaga 720
 agtcaaggac aagggtgtaca gttatgtgaa tactttgtac tctttcttaa ggcacactta 780
 agtaaaagtg tgatttttgt acattacact aaattattag catttgtttt agcattacct 840
 aatctttttt ttttcttctg ttcgtgcaaa ctgtcagctt ttatctcaaa tgcttatttt 900
 aaaagaacag tggaaacctt cttttttcta agtgccagta ttccctgggt tttggactta 960
 aactagcaat gcctgtggaa gagactaaag acctgagact ctgtcttggg atttgggtga 1020
 tgcagttgat tccttgctag ttctcttacc aactgtgaac actgatggga agcaggataa 1080
 tgaagcttcc ggaccatccc tgctctgtgt ccatctactc atccaatgga gtcattagca 1140
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 gaaaagggga aaaaaggaaa aaaaaaaaaa ggcaatggaa aatggtgaaa tccattcagt 1380
 ttccatgtta gctaaattac tgtaagattc ctataatagc ttttcttggg aaggcagacc 1440
 cagtatgaaa tagtaataac catttgggct atattttacat gctactaaat ttttgtaata 1500
 attcaaacaa ctttagcata tataaaaagt tctcataaga attaagtaca aaaaaaaaaa 1560
 aaaaaaa 1567

<210> 33
 <211> 1534
 <212> DNA
 <213> Mus sp.

<400> 33
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 ctgacatttc tcgtgagaat ggtctttcta gtaccagtgt agcaaaggaa tcataaaatt 120
 tgataaaact aagacagttg gattagcagg gaagagaaga ggcacctcct ctgccagcca 180
 tgatgaagga agcatcggag cctctagcca gtgtcaccag catcaataag caagacagta 240
 aagtacagga tggagagata agaaaagaaa aaattggaa catcactcca tcgaaacagc 300
 attcttcagt ccacttcttc ccaaagataa tggattcaga ctccaccacg ctcatcccg 360
 tgtcccgtc attttcccaa gaaatgccaa ttggcttcta ccagatcacc agcaccaga 420
 acagctccac cttatcgccc agaggacagc tggcttctaa atccaccatc ctgagctgct 480
 cccacaaaaga cagcagcctg ggaaagcaga gcaccagctc catggttcca cggaggcagc 540
 cccagtcgag ctctgacgtg gatacgtata cttttgggaa tggtaggat tatttccttt 600
 ctttgttttg agaatcgaag aagctcaccg cccacacacc ccaagccgag aacgtgagcg 660
 aacacctttt tgtgatcctt gaggaagtcg gccaatttac atccagttct ctcgagaaa 720
 ttaaaatagc tgaggttaa atcaagggcc tctttgtgag gcttgtaaac tcctccaatg 780
 aaaaggaaagt agagattgga aaccacattc ttcagcaaaa cgtgaatgga cacgcagctc 840
 ccttgtagca gttccccgac aacatcacac tgcaggccaa ctccacggtg acagtgtggg 900
 cagcagcttc ggaagcaaag ccacagccac caacggactt tggttgggag gaacagagca 960
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cctggtacac tccatccac tggaagcaag cctgggagaa gttagagact gacattgaat 1080
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tctaccctgt cctctacaga gaaaaggaaa tcccgccaac tgtcttacc aataagagcc 1260
cctggtgccg caatcccaac acttctccac atccgtacag ctctctgatt gactcacatg 1320
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aaccagaccc agggaccaag aaaaagaaa caaagtcata agaaaatgga aagccatgaa 1440
atctgtgaac gtgagtaact attgtagagt tgctttataa caaaatattc cacaataaat 1500
tgcaataaat ttttgagggt ctgcctttat gacc 1534

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<210> 34
<211> 1353
<212> DNA
<213> Mus sp.

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<400> 34
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aaatggccaa ttcgttacga ggagaagtac tgactcttta taaaaatctg ctgtatcttg 180
gacgggacta tccaaaagga gcagactatt ttaaaaggcg tttgaagaac gttttcctta 240
aaaacaagga tgtggaggac ccagagaaga tcaaagaact tatcgacga ggagaatttg 300
taatgaagga gctagaggcc ttgtacttcc ttaggaaata cagagctatg aagcaacgtt 360
actattcaga taccaaagtc tgaccaatca ttgcaccagt cgagctgaca accagtgtctg 420
gctgtttgcc tgtaccaact attaaaaaat aattcagttt aaaagggtga gatacatggt 480
ttttaaaaa atgagttgcc ctactgtact gaaatagggt tcaaccttat tgatactgag 540
agctttgccc ataatccttt tattactgaa atagtaactt tagtaccttt catgataata 600
taattttgaa agaaaataca cttaattttt aaacatgtta tagccaattt tcttaagtct 660
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agcttctaga gtgtctttgt ccttgttttt tggtgttttg ttagcccatc tagtatacta 780
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agcaaaaatg tttatgtaat gtttttagca acgttataaa taacatttct aacttaaaaag 1140
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gagcactgac tgctcttcca gaggtcctga atttaattcc cagcaaccat atgggtggctt 1260
acaaccatct gtaatgggat ctgatgtcca cttctgggtg gtctgaacac agacagtgt 1320
ctcatagaat aaataaataa acgaataaat ctt 1353

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<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
primer

```

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<400> 35
gaccaaagcc gagcgactgc ggc

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<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 36
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<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 37
tgacatccgt aaagacctct atgcc 25

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 38
gaggtagcac gtggcggttca cgaa 24